1145-VC-2650 **Tomas Gedeon**, **Bree Cummins** and **Ying Xin*** (yingxinac@gmail.com). *Exploring reversible EMT using DSGRN.* Preliminary report.

Epithelial-to-mesenchymal transition (EMT) and its inverse are essential in many biological processes. Mathematically, one can model the interaction among the regulatory elements as a dynamical system and consider each cell phenotype as an attractor. Previous studies suggested that in addition to E, M states, the network responsible for these phenotypes may also exhibit intermediate phenotypes. The number and importance of such states is subject to intense discussion in EMT community.

Previous modeling efforts used traditional bifurcation analysis to explore such systems by varying one or two parameters at a time. Since the system has tens of parameters that are largely unknown, this limits the range of questions that can be answered.

We present a study where we use computational tool DSGRN (Dynamic Signatures Generated by Regulatory Networks) to explore the dynamics of the network by computing summaries of the dynamics across the whole parameter space. We found that there are parameter regimes where up to 5 additional mixed stable steady states can co-exist with the E and M states. We then explored how various types of perturbations to the system can lead to a monostable M or E state, thus exploring potential pathways between these states in the full parameter space. (Received September 25, 2018)